In the Claims

1. (Original) A method for identifying a research subject, comprising:

obtaining medical data from a subject;

associating an identifier for said subject with said medical data in at least a first database;

associating the identifier for said subject with the name and contact information of said subject;

identifying criteria for selecting a research subject;

extracting an identifier from the first database, wherein said identifier is associated with a subject matching the identified criteria; and

matching the identifier from the first database with the name and contact information in order to identify the research subject.

2. (Original) The method according to claim 1, further comprising obtaining informed consent from said subject, wherein said informed consent permits the medical data to be used to identify said subject as a potential research subject.

3. (Original) The method according to claim 1, wherein medical data are obtained from said subject and associated with the identifier for said subject in at least a first database longitudinally.

4. (Original) The method according to claim 1, wherein said subject is a member of a group of donors, and said method is repeated for each member.

5. (Original) The method according to claim 1, wherein the subject is a deferred donor.

6. (Original) The method according to claim 1, wherein the medical data comprise a medical history.

7. (Original) The method according to claim 1, wherein the medical data comprise a family history.

8. (Original) The method according to claim 1, wherein the medical data comprise clinical chemistry test results.

9. (Original) The method according to claim 1, wherein the medical data comprise pharmacogenomic or genomic data.

10. (Original) The method according to claim 1, wherein the medical data comprise proteomic data.

11. (Original) The method according to claim 1, wherein the criteria include medical history information.

12. (Original) The method according to claim 1, wherein the criteria include family history information.

13. (Original) The method according to claim 1, wherein the criteria include clinical chemistry test results.

14. (Original) The method according to claim 1, wherein the criteria include pharmacogenomic or genomic information.

15. (Original) The method according to claim 1, wherein the criteria include proteomic information.

16. (Original) The method according to claim 1, wherein said first database is a computerized database.

17. (Original) The method according to claim 1, wherein the name and contact information is stored in at least a second database.

18. (Original) The method according to claim 17, wherein said first database and said second database are computerized databases.

19. (Original) The method according to claim 18, wherein the first and second databases are stored on separate computers.

20. (Original) The method according to claim 19, wherein the computer storing the first database is connected through a network firewall with the computer storing the second database.

21. (Currently amended) The method according to claim 1, wherein the first database is a computerized database and is accessible through a network.

22. (Original) The method according to claim 21, wherein the network is a local area network or an intranet.

23. (Original) The method according to claim 21, wherein the network is an internet.

24. (Original) A method for identifying a research subject in a group of donors from at least one collection establishment, comprising:

a. obtaining a biological sample and medical data from a donor;

b. associating an identifier for said donor with said biological sample and medical data in at least a first database;

c. associating the identifier for said blood donor with the name and contact information of said donor;

d. identifying criteria for selecting a research subject;

e. extracting an identifier from the first database, wherein said identifier is associated with a donor matching the identified criteria; and

f. matching the identifier from the first database with the name and contact information in order to identify a research subject.

25. (Original) The method according to claim 24, further comprising obtaining informed consent from said blood donor, wherein said informed consent permits the medical data to be used to identify said blood donor as a potential research subject.

26. (Original) The method according to claim 24, wherein medical data are obtained from said donor and associated with the identifier for said donor in at least a first database longitudinally.

27. (Original) The method according to claim 24, wherein said donor is a deferred donor.

28. (Original) The method according to claim 24, wherein the medical data comprise a medical history.

29. (Original) The method according to claim 24, wherein the medical data comprise a family history.

30. (Original) The method according to claim 24, wherein the medical data comprise clinical chemistry test results.

31. (Original) The method according to claim 24, wherein the medical data comprise pharmacogenomic or genomic data.

32. (Original) The method according to claim 24, wherein the medical data comprise proteomic data.

33. (Original) The method according to claim 24, wherein the criteria include medical history information.

34. (Original) The method according to claim 24, wherein the criteria include family history information.

35. (Original) The method according to claim 24, wherein the criteria include clinical test results.

36. (Original) The method according to claim 24, wherein the criteria include pharmacogenomic or genomic information.

37. (Original) The method according to claim 24, wherein the criteria include proteomic information.

38. (Original) The method according to claim 24, wherein said first database is a computerized database.

39. (Original) The method according to claim 24, wherein the name and contact information of said blood donor is stored in at least a second database.

40. (Original) The method according to claim 39, wherein said first database and said second database are computerized databases.

41. (Original) The method according to claim 40, wherein said first and second databases are stored on separate computers.

42. (Original) The method according to claim 41, wherein the computer storing the first database is connected through a network firewall with the computer storing the second database.

43. (Currently amended) The method according to claim 24, wherein the first database is a computerized database and is accessible through a network.

44. (Original) The method according to claim 43, wherein the network is a local area network or an intranet.

45. (Original) The method according to claim 43, wherein the network is an internet.

46. (Currently amended) The method of claim 1 wherein a [[A]] plurality of biological samples is collected from at least one subject, wherein each sample is associated with an identifier linking said biological sample to at least one of medical data, genomic data, pharmacogenomic data, and proteomic data in at least a first database and wherein said biological samples are collected and stored longitudinally.

47. (Original) The plurality of biological samples according to claim 46, wherein said samples are whole blood, plasma, serum, blood cells, and proteins or nucleic acids isolated therefrom.

48. (Currently amended) The method of claim 4 wherein a [[A]] plurality of biological samples is collected from at least one donor, wherein each sample is collected at a collection establishment and associated with an identifier linking said donor and said biological sample to at least one of medical data, genomic data, pharmacogenomic data, and proteomic data in at least a first database and wherein said plurality of biological samples are collected and stored longitudinally.

49. (Original) A method for creating a database, the method comprising:

a. collecting a biological sample from at least one subject;

b. collecting a medical data from said at least one subject;

c. deriving proteomic information and genomic information from the sample;

d. storing the sample in a location from which the sample can be recovered;

e. associating the medical data, the proteomic information, and the genomic information with an identifier that can be used to locate the sample; and

f. performing steps a to e on the same subject longitudinally; and wherein steps b to d may be performed in any order.

50. (Original) The method according to claim 49, wherein steps a to f are performed on multiple subjects.

51. (Original) The method according to claim 49, wherein the biological sample is whole blood, plasma, serum, blood cells, or proteins or nucleic acids isolated therefrom.

52. (Original) The method according to claim 49, wherein the samples are collected from at least one collection establishment.

53. (Original) The method according to claim 49, wherein said medical data comprises clinical chemistry test information.

54. (Original) The method according to claim 53, wherein the clinical chemistry test is at least one test selected from ABO/RH type, antibody screening tests, alanine aminotransferase (ALT) tests, cytomegalovirus (CMV) screening, hepatitis B screening, hepatitis B core antibody screening, hepatitis C screening, human immunodeficiency virus (HIV) types 1 and 2 screening, human T-cell lymphotropic virus (HTLV)-1 screening, and HIV antigen screening.

55. (Original) The method according to claim 49, wherein the genomic information includes DNA polymorphisms.

56. (Original) The method according to claim 49, wherein the DNA polymorphisms are single nucleotide polymorphisms.

57. (Original) The method according to claim 49, wherein the proteomic information includes the proteins expressed in the sample.

58. (Original) The method according to claim 49, wherein the genomic information includes the ribonucleic acids expressed in the sample.

59. (Original) The method according to claim 49, wherein said medical data comprises family histories from the subjects.

60. (Original) The method according to claim 49, wherein said medical data comprises demographic information from the subjects.

61. (Original) The method according to claim 49, wherein at least one of the medical data, the genomic information, the proteomic information, and the location for the sample is associated with an identifier for the subject that can be used to retrieve the name and contact information of said subject.

62. (Currently amended) A method for identifying a genomic or a proteomic characteristic which correlates with a disease, said method comprising:

creating a database according to claim [[48]] 49;

identifying subjects with the disease;

identifying genomic and proteomic characteristics shared by said subjects.

63. (Original) The method according to claim 62, wherein the genomic characteristic identified is a single nucleotide polymorphism.

64. (Original) The method according to claim 62, wherein the genomic characteristic identified is pharmacogenomic information.

65. (Original) The method according to claim 62, wherein the proteomic information is a change in protein level.

66. (Original) A method for recruiting a research subject for a clinical study, said method comprising:

identifying said research subject according to claim 1 according to selected criteria; and

contacting said research subject for recruiting said research subject for said clinical study.

67. (Original) A method for recruiting a research subject for a clinical study, said method comprising:

identifying said research subject according to claim 24 according to selected criteria; and

contacting said research subject for recruiting said research subject for said clinical study.

68. (Original) The method according to claim 27, wherein said deferred donor is a deferred blood or plasma donor.